

SEQ. ID 3-1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAAACAGTTTTGAAGGATCT 60
 SEQ. ID 4-1 M T F N S F E G S 9

61 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA 120
 10 K T C V P A D I N K E E E F V E E F N R 29

121 TTA AAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACGA 180
 30 L K T F A N F P S G S P V S A S T L A R 49

181 GCAGGGTTTCTTTATACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTCATGCAGCT 240
 50 A G F L Y T G E G D T V R C F S C H A A 69

241 GTAGATAGATGGCAATATGGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT 300
 70 V D R W Q Y G D S A V G R H R K V S P N 89

301 TGCAGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCACGCAGTCTACAAATTCTGGT 360
 90 C R F I N G F Y L E N S A T Q S T N S G 109

361 ATCCAGAATGGTCAGTACAAAGTTGAAAACATCTGGGAAGCAGAGATCATTTTGCCTTA 420
 110 I Q N G Q Y K V E N Y L G S R D H F A L 129

421 GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATA 480
 130 D R P S E T H A D Y L L R T G Q V V D I 149

481 TCAGACACCATATACCCGAGGAACCTGCCATGTATaGTGAAGAAGCTAGATTAAAGTCC 540
 150 S D T I Y P R N P A M Y S E E A R L K S 169

541 TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTGCTGGACTC 600
 170 F Q N W P D Y A H L T P R E L A S A G L 189

601 TACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGTGTGGTGGAAAACGAAAAAT 660
 190 Y Y T G I G D Q V Q C F C C G G K L K N 209

661 TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTGCTTCTTT 720
 210 W E P C D R A W S E H R R H F P N C F F 229

721 GTTTTGGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780
 230 V L G R N L N I R S E S D A V S S D R N 249

781 TTCCCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC 840
 250 F P N S T N L P R N P S M A D Y E A R I 269

841 TTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTT 900
 270 F T F G T W I Y S V N K E Q L A R A G F 289

901 TATGCTTTAG^{1,2}GTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGCTAACTGAT 960
 290 Y A L G E G D K V K C F H C G G G L T D 309

961 TGGAAGCCCACTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGG^{2,3}TGCAAAATAT 1020
 310 W K P S E D P W E Q H A K W Y P G C K Y 329

1021 CTGTTAGAACAGAAGGGACAAGAATATATAAACAATATTCATTTAACTCATTCACTTGAG 1080
 330 L L E Q K G Q E Y I N N I H L T H S L E 349

Fig. 1

1081 GAGTGTCTG³GTAAGAACTACTGAGAAAACACCATCACTAACTAGAAGAATT⁴GATGATAACC 1140
 350 E C L V R T T E K T P S L T R R I D D T 369
 1141 ATCTTCCAAAATCCTATGGTACAAGAAGCTATACGAATGGGGTTCAGTTTCAAGGACATT 1200
 370 I F Q N P M V Q E A I R M G F S F K D I 389
 1201 AAGAAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT 1260
 390 K K I M E E K I Q I S G S N Y K S L E V 409
 1261 CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320
 410 L V A D L V N A Q K D S M Q D E S S Q T 429
 1321 TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGGAGAAGCTT 1380
 430 S L Q K E I S T E E Q L R R L Q E E K L 449
 1381 TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTC 1440
 450 C K I C M D R N I A I V F V P C G H L V 469
 1441 ACTTGTAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT 1500
 470 T C K Q C A E A V D K C P M C Y T V I T 489
 1501 TTCAAGCAAAAAATTTTTATGTCTTAATCTAACTCTATAGTAGGCATGTTATGTTGTTCT 1560
 490 F K Q K I F M S * 497
 1561 TATTACCTGATTGAATGTGTGATGTGAAGTACTTTAAGTAATCAGGATTGAATTCCAT 1620
 1621 TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTTTTAGTTGGCAATATA 1680
 1681 ATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTTACTGTTA 1740
 1741 TTTAATTGAAACCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATGTGT 1800
 1801 ATTCATAGTATACTGATTTAATTTCTAAGTGAAGTGAATTAATCATCTGGATTTTTTAT 1860
 1861 TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
 1921 ATCTCCCAATCACATAATTTGTTTTGTGTGAAAAAGGAATAAATTGTTCCATGCTGGTG 1980
 1981 GAAAGATAGAGATTGTTTTAGAGTTGGTTGTTGTTTTAGGATTCTGTCCATTTTTCT 2040
 2041 TTTAAAGTTATAAACACGTAATTGTGCGAATTATTTTTTAAAGTGATTGGCATTTTTG 2100
 2101 AAAGCGTATTTAATGATAGAATACTATCGAGCCAACATGTACTGACATGGAAAGATGTCA 2160
 2161 AAGATATGTTAAGTGTAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA 2220
 2221 AAGTATGTATGTTTTTAATATGCATAGAACAAAAGATTTGGAAAGATATACACCAAACTG 2280
 2281 TTAAATGTGGTTTCTCTTCGGGGAGGGGGGATTGGGGGAGGGGCCCCAGAGGGGTTTTA 2340
 2341 TAGGGGCCTTTTCACTTTCTACTTTTTTCATTTTTGTCTGTTTGAATTTTTTATAAGTAT 2400
 2401 GTATTACTTTTGTAATCAGAAATTTTAGAAAGTATTTTGCTGATTTAAAGGCTTAGGCAT 2460
 2461 GTTCAAACGCCTGCAAACTACTTATCACTCAGCTTTAGTTTTTCTAATCCAAGAAGGCA 2520
 2521 GGGCAGTTAACCTTTTTGGTGCCAATGTGAAATGTAATGATTTTATGTTTTTCTGCTT 2580
 2581 TGTGGATGAAAAATATTTCTGAGTGGTAGTTTTTGGACAGGTAGACCATGTCTTATCTTG 2640
 2641 TTTCAAAATAAGTATTTCTGATTTTGTAAATGAAATATAAAATATGTCTCAGATCTTCC 2700
 2701 AATTAATTAGTAAGGATTCATCCTTAATCCTTGCTAGTTTAAAGCCTGCCTAAGTCACTTT 2760
 2761 ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTGAGCTTATGTAGGTAAAGT 2820
 2821 AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTCTCA 2880
 2881 TATCATCTGTATCTTAAAGTTTCATGTGAGTTTTTACCGTTAGGATGATTAAGATGTAT 2940
 2941 ATAGGACAAAATGTTAAGTCTTCTCTACCTACATTTGTTTTCTTGGCTAGTAATAGTA 3000
 3001 GTAGATACTTCTGAAATAAATGTTCTCTCAAGATCCTTAAACCTCTTGGAAATTATAAA 3060

Fig. 1 (cont.)

3061 AATATTGGCAAGAAAAGAAGAAATAGTTGTTTAAATATTTTTTAAAAAAACACTTGAATAAG 3120
 3121 AATCAGTAGGGTATAAACTAGAAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACAT 3180
 3181 TACAAGATTCTCACAACAAACCCATTGTAGAGGTGAGTAAGGCATGTTACTACAGAGGAA 3240
 3241 AGTTTGAGAGTAAACTGTAAAAAATTATATTTTTTGTGTACTTTCTAAGAGAAAGAGTA 3300
 3301 TTGTTATGTTCTCCTAATTCTGTTGATTACTACTTTAAGTGATATTCATTTAAACATT 3360
 3361 GCAAATTTATTTTATTTATTTAATTTTCTTTTTGAGATGGAGTCTTGCTTGTCACCCAGG 3420
 3421 CTGGAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCTTCTGGGTTCAAGCGAT 3480
 3481 TCTCGTGCTCAGCTTCCTGAGTAGCTGGAATTACAGGCAGGTGCCACCATGCCCGACTA 3540
 3541 ATTTTTTTTTATTTTTAGTAGAGACGGGGTTTACCATTGTTGGCCAGGCTGGTATCAAAC 3600
 3601 TCCTGACCTCAAGAGATCCACTCGCCTTGCCCTCCCAAAGTGCTGGGATTACAGGCTTGA 3660
 3661 GCCACCACGCCCCGGCTAAAACATTGCAAATTTAAATGAGAGTTTTAAAAATTAAATAATG 3720
 3721 ACTGCCCTGTTTCTGTTTTAGTATGTAAATCCTCAGTTCCTTACCTTTGCACTGTCTGCC 3780
 3781 ACTTAGTTTGGTTATATAGTCATTAACCTTGAATTTGGTCTGTATAGTCTAGACTTTAAAT 3840
 3841 TTAAAGTTTCTACAAGGGGAGAAAAGTGTTAAAAATTTTTAAATATGTTTCCAGGACA 3900
 3901 CTTCACTTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTTAGCCAAGGACTCAAGGACTG 3960
 3961 AATTGTTTTAAACATAAGGCTTTTCTGTTCTGGGAGCCGCACTTCATTAATAATCTTCTA 4020
 4021 AAACCTGTATGTTTAGAGTTAAGCAAGACTTTTTTCTTCTCTCCATGAGTTGTGAAAT 4080
 4081 TTAATGCACAACGCTGATGTGGCTAACAAAGTTTATTTTAAAGAATTGTTTAGAAATGCTGT 4140
 4141 TGCTTCAGGTTCTTAAATCACTCAGCACTCCAACCTTCTAATCAAATTTTTGGAGACTTA 4200
 4201 ACAGCATTTGTCTGTGTTTGAACATAAAAAAGCACCGGATCTTTTCCATCTAATTCGCA 4260
 4261 AAAATTGATCATTTGCAAAAGTCAAAACATATAGCCATATCCAAATCTTTTCCCCCTCCAA 4320
 4321 GAGTTCTCAGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTCACTCTAGGATTT 4380
 4381 CAAGTCACCACCTTATTTTACATTTTAGTCATGCAAAGATTCAAGTAGTTTTGCAATAAGT 4440
 4441 ACTTATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAGCATTGTCTTAATTTTTGAG 4500
 4501 AACTGGTTTTAGCATTTACAACTAAATTCAGTTAATTAATTAATAGCTTTATATTGCC 4560
 4561 TTTCTCTGCTACATTTGGTTTTTTCCCTGTCCCTTGATTACGGGCTAAGGTAGGGTAAG 4620
 4621 AXXGGGTGTAGTGAGTGTATATAATGTGATTTGGCCCTGTGTATTATGATATTTTGTAT 4680
 4681 TTTTGTGTTATATTATTTACATTTTCAAGTGTGTTTTTGTGTTTCCATTTTAGGGGAT 4740
 4741 AAAATTTGTATTTTGAATATGAATGGAGACTACCGCCCCAGCATTAGTTTACATGATA 4800
 4801 TACCCTTTAAACCGAATCATTGTTTTATTTCTGATTACACAGGTGTTGAATGGGGAAA 4860
 4861 GGGGCTAGTATATCAGTAGGATATACTATGGGATGTATATATATCATTGCTGTTAGAGAA 4920
 4921 ATGAAATAAAATGGGGCTGGGCTCAGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGG 4980
 4981 CTGAGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC 5040
 5041 CCCGTCTCTACTAAAAACAGAAAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGTCCCA 5100
 5101 GCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCAGAGCTTGCAGTGA 5160
 5161 GCCGAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAA 5220
 5221 AAAAAAAAAAAG 5232

Fig. 1 (cont.)

SEQ. ID 5-1 TTGCTCTGTCACCCAGTTTGGAGTGCAGTTATGCAGTCTCACACTGCAAGCTCTGCCTCA 60
61 TGGGCTCAAGTGAACCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACCACAGGCAGGTGCC 120
121 ACCATGTCTGGCTAATTTTTGAGTTTCTTTGTAGAGATGGTGTCTTGGCAAGTCACCCAG 180
181 TTTGAGGCTGGTCTCAAAACACCTGGGCTCAAGCAATCCATCTACCTCAGCCTCCCAAAGT 240
241 GCTGGGATTACAGGAGTGAGCCATGGCATGAGGCCTTGTGGGGTGTCTCTTTTAAATGAA 300
301 AGCATACTCTGTTTACGTATTTGATATGAAGCAATATCCTTCCCTTCCACAAAGACAAAA 360
361 ATTATCCTATTTTTCTCAAAACATATGTCTTTTTCTCTACTTTTTCATTTTTGTACTTT 420
421 TGATGGACACATGTGTTACATTGATTTCACTTTCTCATAATTCTGCTGTAAGAAAAACAA 480
481 TAGTGCCAGTTCAATGACAAATAGCAACAGTCTGTTATTGCTAGACTGTTACTGTTAGTG 540
541 GAGACTACCAGAACAGTCAGTCCCAGTGTGAGGGAATCAAAGAGAACATGTTCCCTCTCT 600
601 AAAGGGCACAGCTGCTGCTCAGCTTTAGCTGATTGCTGCCCTGCAGGACTATAGGCCAG 660
661 TGTGCTAGATCTTTGATGTTTCAAGAGAAGCTTGAATCTAGAATGTGATGGGAAGTC 720
721 TCTTACATTTAAACATGTTGGCAATTAATGGTAAGATTTAAAAATACTGTGGTCCAAGAA 780
781 AAAAATGGATTTGGAACTGGATTAAATTCAAATGAGGCATGCAGATTAATCTACAGCAT 840
841 GGTACAATGTGAATTTCTGGTTCTTTAATTGCAGTGAATTAGGTAAGATGTTAGCTT 900
901 TGGGGAAGCTAAGTGCAGAGTATGCAGAACTATTATTTTGTAAAGTTTTCTCTAAGTAT 960
961 AAATAAATTTCAAAATAAAAAATAAAAACTTAGTAAAGAACTATAATGCAATTCTATGTAA 1020
1021 GCCAAACATAATATGTCTTCCAGTTTGAAACCTCTGGGTTTTATTTTATTTTATTTTATT 1080
1081 TTTGAGACAGAGTCTTGCTGTGTCACCCAGGCTGGAGTGTAGTGGCACTATTTGGGCCA 1140
1141 CTGCAACCTCCACCTCCAGGCTCAAATGATTCTCCTGCCCTCAGCCTCCGGAGTAGCTGG 1200
1201 GATTACAGGCGCGTACCACCACACCCAGCTAATTTTTGTATTTTGTAGATAGATGGGGTT 1260
1261 TCACCATTTTGGCCAGGCTGGTTTGAATCCTGACCTCAAGTGATCCACTGTCTTGGC 1320
1321 CTCCCAAATGCTGGGATTACAGGCGTGAGCCACTGCACCAGGCAGAGCCTCTGTTTTT 1380
1381 TATCTCTTTTGGCCTCTACAGTGCTTAGTAAAGCACCTGATACATGGTAAACGATCAGT 1440
1441 AATTACTAGTACTCTATTTTGGAGAAAATGATTTTTTAAAAAGTCATTGTGTTCCATCCA 1500
1501 TGAGTCGTTTGAAGTTTTAAACTGTCTTTTGTGTTTTTGAACAGGTTTACAAAGGAG 1560
1561 GAAAACGACTTCTTCTAGATTTTTTTTTCAGTTTCTTCTATAAATCAAACATCTCAAAA 1620
1621 TGGAGACCTAAAATCCTTAAAGGGACTTAGTCTAATCTCGGGAGGTAGTTTGTGCATGG 1680
1681 GTAAACAAATTAAGTATTAACCTGGTGTTTACTATCCAAAGAATGCTAATTTTATAAACA 1740
1741 TGATCGAGTTATATAAGGTATACCAATAGAGTTTGATTTTGAATTTGATTTGTGGAAAT 1800
1801 AAAGGAAAAGTGATTCTAGCTGGGGCATATTGTTAAAGCATTTTTTTTCAGAGTTGGCCAG 1860
1861 GCAGTCTCTACTGGCACATTCTCCCATATGTAGAATAGAAATAGTACCTGTGTTGGG 1920
1921 AAAGATTTTAAAATGAGTGACAGTTATTTGGAACAAAGAGCTAATAATCAATCCACTGCA 1980
1981 AATTAAAGAAACATGCAGATGAAAGTTTGACACATTAATAACTTCTACAGTGACAAA 2040
2041 AAAATCAAGAACAAAGCTTTTTGATATGTGCAACAAATTTAGAGGAAGTAAAGATAA 2100
2101 ATGTGATGATTGGTCAAGAAATTATCCAGTTATTTTACAAGGCCACTGATATTTTAAACGT 2160
2161 CCAAAGTTTGTTTAAATGGGCTGTTACCGCTGAGAATGATGAGGATGAGAATGATGGTT 2220
2221 GAAGGTTACATTTTAGGAAATGAAGAACTTAGAAAATTAATATAAAGACAGTGATGAAT 2280
2281 ACAAAGAAGATTTTTATAACAATGTGTAAATTTTTGGCCAGGGAAAGGAATATTGAAGT 2340
2341 TAGATACAATTACTTACCTTTGAGGGAATAATTGTTGGTAATGAGATGTGATGTTCTC 2400
2401 CTGCCACCTGGAAACAAAGCATTGAAGTCTGCAGTTGAAAAGCCCAACGTCTGTGAGATC 2460
2461 CAGGAAACCATGCTTGCAAACTGCTGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAG 2520
2521 TGACTTGCTTATTGGTCATTGCTAGTATTATCGACTCAGAACCTCTTTACTAATGGCTAG 2580
2581 TAAATCATAATTGAGAAATTCTGAATTTTGACAAGGTCTCTGCTGTTGAAATGGTAAATT 2640
2641 TATTATTTTTTTTTGTCATGATAAATCTGGTTCAAGGTATGCTATCCATGAAATAATTC 2700
2701 TGACCAAACTAAATTGATGCAATTTGATTATCCATCTTAGCCTACAGATGGCATCTGGT 2760
2761 AACTTTTGACTGTTTTAAAAATAAATCCACTATCAGAGTAGATTTGATGTTGGCTTCAG 2820
2821 AAACATTTAGAAAAACAAAGTTCAAAAATGTTTTCAGGAGGTGATAAGTTGAATAACTC 2880
2881 TACAATGTTAGTTCTTTGAGGGGGACAAAAATTTAAATCTTTGAAAGGTCTTATTTTA 2940
2941 CAGCCATATCTAATTATCTTAAGAAAATTTTTAACAAAGGGAATGAAATATATATCATG 3000
3001 ATTCTGTTTTTCCAAAGTAACCTGAATATAGCAATGAAGTTTCAGTTTTGTATTGGTAG 3060
3061 TTTGGGCAGAGTCTCTTTTTGCAGCACCTGTTGTCTACCATAATTACAGAGGACATTTCC 3120
3121 ATGTTCTAGCCAAGTATACTATTAGAATAAARAACTTAACATTGAGTTGCTTCAACAGC 3180

Fig. 2

3181 ATGAAACTGAGTCCAAAAGACCAAATGAACAAACACATTAATCTCTGATTATTTATTTTA 3240
 3241 AATAGAATATTTAATTGTGTAAGATCTAATAGTATCATTATACTTAAGCAATCATATTCC 3300
 3301 TGATGATCTATGGGAAATAACTATTATTTAATTAATTGAAAACAGGTTTTAAGATGTG 3360
 3361 TTAGCCAGTCCCTGTTACTAGTAAATCTCTTTATTTGGAGAGAAAATTTAGATTGTTTTGT 3420
 3421 TCTCCTTATTAGAAGGATTGTAGAAAAGAAAAAATGACTAATTGGAGAAAAATTTGGGGAT 3480
 3481 ATATCATATTTCACTGAATTCAAAATGTCTTCAGTTGTAAATCTTACCATTATTTTACGT 3540
 3541 ACCTCTAAGAAATAAAAGTGCTTCTAATTAATAATATGATGTCATTAATTATGAAATACTT 3600
 3601 CTTGATAACAGAAGTTTTAAATAGCCATCTTAGAATCAGTGAAATATGGTAATGTATTA 3660
 3661 TTTTCTCCTTTGAGTNAGGTCTTGTGCTTTTTNTTCTGGCCACTAAATNTCACCATNT 3720
 3721 CCAANAAGCAAANTAAACCTATTCTGAATATTTTTGCTGTGAAACACTTGNACAGCAGAGC 3780
 3781 TTTCCCNCCATGNNAGAAGCTTCATGAGTCACACATTACATCTTTGGGTTGATTGAATGC 3840
 3841 CACTGAAACATTTCTAGTAGCCTGGAGNAGTTGACCTACCTGTGGAGATGCCTGCCATTA 3900
 3901 AATGGCATCCTGATGGCTTAATACACATCACTCTTCTGTGNAGGGTTTTAATTTTCAACA 3960
 3961 CAGCTTACTCTGTAGCATCATGTTACATTGTATGTATAAAGATTATACNAAGGTGCAAT 4020
 4021 TGTGTATTTCTTCTTAAATGTATCAGTATAGGATTTAGAATCTCCATGTTGAAACTCT 4080
 4081 AAATGCATAGAAATAAAATAAAAAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTA 4140
 4141 AACTGATAAAAGCAAAGCCATGCACAAAACCTCCCTAGAGAAAGGCTAGTCCCTTT 4200
 4201 TCTTCCCATTCATTTTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAATTTGA 4260
 SEQ. ID 6-1 M N I V E N S I F L S N L M 14
 4261 TGAAAAGCGCCAACACGTTTGAACCTGAAATACGACTTGTCTGTAAGTGTACCGAATGT 4320
 15 K S A N T F E L K Y D L S C E L Y R M S 34
 4321 CTACGTATTCCACTTTTCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGCTG 4380
 35 T Y S T F P A G V P V S E R S L A R A G 54
 4381 GTTTCTATTACACTGGTGTGAATGACAAGGTCAAATGCTTCTGTTGTGGCCTGATGCTGG 4440
 55 F Y Y T G V N D K V K C F C C G L M L D 74
 4441 ATAAGTGGAAAAGAGGAGACAGTCTTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCA 4500
 75 N W K R G D S P T E K H K K L Y P S C R 94
 4501 GATTCGTTTCAGAGTCTAAATTCCGTTAACAACCTTGAAGCTACCTCTCAGCCTACTTTTC 4560
 95 F V Q S L N S V N N L E A T S Q P T F P 114
 4561 CTTCTTCAGTAACACATTCCACACACTCATTACTTCCGGGTACAGAAAACAGTGGATATT 4620
 115 S S V T H S T H S L L P G T E N S G Y F 134
 4621 TCCGTGGCTCTTATTCAAACCTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGAAT 4680
 135 R G S Y S N S P S N P V N S R A N Q E F 154
 4681 TTTCTGCCTTGATGAGAAGTTCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTAC 4740
 155 S A L M R S S Y P C P M N N E N A R L L 174
 4741 TTAATTTTCAGACATGGCCATTGACTTTTCTGTGCGCAACAGATCTGGCACGAGCAGGCT 4800
 175 T F Q T W P L T F L S P T D L A R A G F 194
 4801 TTTACTACATAGGACCTGGAGACAGAGTGGCTTGCTTTGCCTGTGGTGGAAAATTGAGCA 4860
 195 Y Y I G P G D R V A C F A C G G K L S N 214
 4861 ATTGGGAACCGAAGGATAATGCTATGTCAGAACACCTGAGACATTTTCCCAAATGCCCAT 4920
 215 W E P K D N A M S E H L R H F P K C P F 234

Fig. 2 (cont.)

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4921 TTATAGAAAATCAGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGA 4980
 235 I E N Q L Q D T S R Y T V S N L S M Q T 254

4981 CACATGCAGCCCCGCTTTAAACATTCTTTAACTGGCCCTCTAGTGTCTAGTTAATCCTG 5040
 255 H A A R F K T F F N W P S S V L V N P E 274

5041 AGCAGCTTGCAAGTGC GG G T T T T T A T T A T G T G G T A A C A G T G A T G T C A A A T G C T T T T 5100
 275 Q L A S A G F Y Y V G N S D D V K C F C 294

5101 GCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGTTCAACATGCCA 5160
 295 C D G G L R C W E S G D D P W V Q H A K 314

5161 AGTGGTTTCCAAGGTGTGAGTACTTGATAAGAATTAAAGGACAGGAGTTCATCCGTCAAG 5220
 315 W F P R C E Y L I R I K G Q E F I R Q V 334

5221 TTCAAGCCAGTTACCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCCAGGAG 5280
 335 Q A S Y P H L L E Q L L S T S D S P G D 354

5281 ATGAAAATGCAGAGTCATCAATTATCCATTTTGAACCTGGAGAAGACCATTGAGAAGATG 5340
 355 E N A E S S I I H F E P G E D H S E D A 374

5341 CAATCATGATGAATACTCCTGTGATTAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCC 5400
 375 I M M N T P V I N A A V E M G F S R S L 394

5401 TGGTAAAACAGACAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAATTATAGACTAGTCA 5460
 395 V K Q T V Q R K I L A T G E N Y R L V N 414

5461 ATGATCTTGTGTTAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGGAGAGAGAAA 5520
 415 D L V L D L L N A E D E I R E E E R E R 434

5521 GAGCAACTGAGGAAAAAGAATCAATGATTATTATTATTAATCCGGAAGAATAGAATGGCAC 5580
 435 A T E E K E S N D L L L I R K N R M A L 454

5581 TTTTTCACATTTGACTTGTGTAATCCAATCCTGGATAGTCTACTAACTGCCGGAATTA 5640
 455 F Q H L T C V I P I L D S L L T A G I I 474

5641 TTAATGAACAAGAACATGATGTTATTAAACAGAAGACACAGACGTCTTTACAAGCAAGAG 5700
 475 N E Q E H D V I K Q K T Q T S L Q A R E 494

5701 AACTGATTGATACGATTTTGTAGTAAAGGAAATATTGCAGCCACTGTATTGAGAACTCTC 5760
 495 L I D T I L V K G N I A A T V F R N S L 514

5761 TGCAAGAAGCTGAAGCTGTGTTATATGAGCATTTATTTGTCGAACAGGACATAAAATATA 5820
 515 Q E A E A V L Y E H L F V Q Q D I K Y I 534

5821 TTCCACAGAAGATGTTTCAGATCTACCAGTGAAGAACAATTGCGGAGACTACAAGAAG 5880
 535 P T E D V S D L P V E E Q L R R L Q E E 554

5881 AAAGAACATGTAAAGTGTGTATGGACAAAGAAGTGTCCATAGTGTGTTTATTCCTTGTGGTC 5940
 555 R T C K V C M D K E V S I V F I P C G H 574

5941 ATCTAGTAGTATGCAAAGATTGTGCTCCTTCTTTAAGAAAGTGTCTATTTGTAGGAGTA 6000
 575 L V V C K D C A P S L R K C P I C R S T 594

Fig. 2 (cont.)

6001 CAATCAAGGGTACAGTTCGTACATTTCTTTTCATGAAGAAGAACCAAAACATCGTCTAAAC 6060
595 I K G T V R T F L S * 604

6061 TTTAGAATTAATTTATTAAATGTATTATAACTTTAACTTTTATCCTAATTTGGTTTCCTT 6120
6121 AAAATTTTTATTTATTACAACTCAAAAAACATTGTTTTGTGTAACATATTTATATATGT 6180
6181 ATCTAAACCATATGAACATATATTTTTTAGAACTAAGAGAATGATAGGCTTTTGTTCCTT 6240
6241 ATGAACGAAAAAGAGGTAGCACTACAAACACAATATTCAATCAAAATTTAGCATTATTG 6300
6301 AAATTGTAAGTGAAGTAAACTTAAGATATTTGAGTTAACCTTTAAGAATTTTAAATATT 6360
6361 TTGGCATTGTACTAATACCGGAACATGAAGCCAGGTGTGGTGGTATGTGCCTGTAGTCC 6420
6421 CAGGCTGAGGCAAGAGAATTACTTGAGCCCAGGAGTTTGAATCCATCCTGGGCAGCATA 6480
6481 TGAGACCCTGCCTTTAAAAACAAACAGAACAAAAACAAACACCAGGGACACATTTCTCT 6540
6541 GTCTTTTTTGATCAGTGTCTTATACATCGAAGGTGTGCATATATGTTGAATCACATTTTA 6600
6601 GGGACATGGTGTTTTTATAAGAATTCTGTGAGAAAAATTTAATAAAGCAACCAAAAAA 6660
6661 AAAAAAAA 6669

Fig. 2 (cont.)

T0600T" 26St4660

SEQ. ID 7-1 GAGCGCCCGGG^{1,2}CTGATCCGAGCCGAGCGGGCCGTATCTCCTTGTCGGCGCCGCTGATTCC 60
 61 CGGCTCTGCGGAGGCCTCTAGGCAGCCGCGCAGCTCCCGTGTGCTGCGCCCGCACTGC 120
 121 ^{2,3}GATTTACAACCTGAAGAATCTCCCTATCCCTATTTTGTCCCCCTGCAGTAATAAATCCC 180
 181 ATTATGGAGATCTCGAACTTTATAAAGGGATATAGTTTGAATTCTATGGAGTGTAAATTT 240
 241 TGTGTATGAATTATATTTTTTAAACATTGAAGAGTTTTTCAGAAAGAAGGCTAGTAGAGTT 300
 301 GATTACTGATACTTTATGCTAAGCAGTACTTTTTTGGTAGTACAATATTTTGTAGGCGT 360
 361 TTCTGATAACACTAGAAAGGACAAGTTTTATCTTGTGATAAATTGATTAATGTTTACAAC 420
 421 ATGACTGATAATTATAGCTGAATAGTCCTTAAATGATGAACAGGTTATTTAGTTTTTAAA 480
 481 TGCAGTGTA AAAAGTGTGCTGTGGAATTTTATGGCTAACTAAGTTTATGGAGAAAATAC 540
 541 CTTCAAGTTGATCAAGAATAATAGTGGTATACAAAGTTAGGAAGAAAGTCAACATGATGCT 600
 601 GCAGGAAATGGAACAAATACAAATGATATTTAACAAGATAGAGTTTACAGTTTTTGAA 660
 661 CTTTAAGCCAAATTCATTTGACATCAAGCACTATAGCAGGCACAGGTTCAACAAAGCTTG 720
 721 TGGGTATTGACTTCCCCCAAAGTTGTGAGCTGAAGTAATTTAGCCCACTAAGTAAATA 780
 781 CTATGATGATAAGCTGTGTGAACCTAGCTTTTAAATAGTGTGACCATATGAAGTTTTAA 840
 841 TTACTTTTGTGTTATTGGAATAAATGAGATTTTTTGGGTGTCATGTTAAAGTGCTTATA 900
 901 GGGAAAGAAGCCTGCATATAATTTTTTACCTTGTCGCATAATCAGTAATTGGTCTGTTAT 960
 961 TCAGGCTTCATAGCTTGTAACCARATATAAATAAAAGGCATAATTTAGGTATTCTATAGT 1020
 1021 TGCTTAGAATTTTGTTAATATAAATCTCTGTGAAAAATCAAGGAGTTTTAATATTTTCAG 1080
 1081 AAGTGCATCCACCTTTTCAAGGCTTTAAGTTAGTATTAAGTCAAGATTATGAACAAATAGC 1140
 1141 ACTTAGGTTACCTGAAAGAGTTACTACAACCCCAAAGAGTTGTGTTCTAAGTAGTATCTT 1200
 1201 GGTAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAATCCAGTAAAGAA 1260
 1261 AGTGTAGTAAATTTACATAAGAGTCTATCATTGATTTCTTTTGTGGTAAAAATCTTAG 1320
 1321 TTCATGTGAAGAAATTTTCATGTGAATGTTTTAGCTATCAAACAGTACTGTCACCTACTCA 1380
 1381 TGCACAAAACCTGCCTCCCAAAGACTTTTCCAGGTCCTCGTATCAAAACATTAAGAGTA^M 1440
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 1441 TAATGGAAGATAGCAGCATCTTGTGAGATTGGACAAACAGCAACAAACAAAAATGAAGT 1500
 22 M E D S T I L S D W T N S N K Q K M K Y 41
 1501 ATGACTTTTCTGTGAACTCTACAGAATGTCTACATATTCAACTTTCCCGCCGGGGTGC 1560
 42 D F S C E L Y R M S T Y S T F P A G V P 61
 1561 CTGTCTCAGAAAGGAGTCTTGCTCGTGGTGTGTTTATTATACTGGTGTGAATGACAAGG 1620
 62 V S E R S L A R A G F Y Y T G V N D K V 81
 1621 TCAATGCTTCTGTTGTGGCCTGATGCTGGATAACTGGAACTAGGAGACAGTCCTATTC 1680
 82 K C F C C G L M L D N W K L G D S P I Q 101
 1681 AAAAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTTCAGAACTGGTTTCAGCTAGTC 1740
 102 K H K Q L Y P S C S F I Q N L V S A S L 121
 1741 TGGGATCCACCTCTAAGAATACGTCTCCAATGAGAAACAGTTTTGCACATTCATTATCTC 1800
 122 G S T S K N T S P M R N S F A H S L S P 141
 1801 CCACCTTGGAACATAGTAGCTTGTTCAGTGGTCTTACTCCAGCCTTTCTCAAACCTTC 1860
 142 T L E H S S L F S G S Y S S L S P N P L 161
 1861 TTAATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAA 1920
 162 N S R A V E D I S S S R T N P Y S Y A M 181
 1921 TGAGTACTGAAGAAGCCAGATTTCTTACCTACCATATGTGGCCATTAACTTTTTTGTAC 1980
 182 S T E E A R F L T Y H M W P L T F L S P 201

Fig. 3

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1981 CATCAGAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGGTAGCCTGCT 2040
 202 S E L A R A G F Y Y I G P G D R V A C F 221

2041 TTGCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAGGATGATGCTATGTCAGAACACC 2100
 222 A C G G K L S N W E P K D D A M S E H R 241

2101 GGAGGCATTTTCCCAACTGTCCATTTTGGAAAATTCTCTAGAACTCTGAGGTTTAGCA 2160
 242 R H F P N C P F L E N S L E T L R F S I 261

2161 TTTCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACATTTATGTACTGGCCAT 2220
 262 S N L S M Q T H A A R M R T F M Y W P S 281

2221 CTAGTGTTCCAGTTCAGCCTGAGCAGCTTGCAAGTGCTGGTTTTTATTATGTGGTTCGCA 2280
 282 S V P V Q P E Q L A S A G F Y Y V G R N 301

2281 ATGATGATGTCAAATGCTTTTGTGTGATGGTGGCTTGAGGTGTTGGGAATCTGGAGATG 2340
 302 D D V K C F C C D G G L R C W E S G D D 321

2341 ATCCATGGGTAGAACATGCCAAGTGGTTTCCAAAGTGTGAGTTCTTGATACGAATGAAAG 2400
 322 P W V E H A K W F P R C E F L I R M K G 341

2401 GCCAAGAGTTTGTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTTGT 2460
 342 Q E F V D E I Q G R Y P H L L E Q L L S 361

2461 CAACTTCAGATACCACTGGAGAAGAAAATGCTGACCCACCAATTATTCATTTTGGACCTG 2520
 362 T S D T T G E E N A D P P I I H F G P G 381

2521 GAGAAAGTTCTTCAGAAGATGCTGTGATGATGAATACACCTGTGGTTAAATCTGCCTTGG 2580
 382 E S S S E D A V M M N T P V V K S A L E 401

2581 AAATGGGCTTTAATAGAGACCTGGTGAAACAAACAGTTCAAAGTAAATCCTGACAACTG 2640
 402 M G F N R D L V K Q T V Q S K I L T T G 421

2641 GAGAGAACTATAAAACAGTTAATGATATTGTGTCAGCACTTCTTAATGCTGAAGATGAAA 2700
 422 E N Y K T V N D I V S A L L N A E D E K 441

2701 AAAGAGAAGAGGAGAAGGAAAAACAAGCTGAAGAAATGGCATCAGATGATTTGTCATTAA 2760
 442 R E E E K E K Q A E E M A S D D L S L I 461

2761 TTCGGAAGAACAGAATGGCTCTCTTTCAACAATTGACATGTGTGCTTCCTATCCTGGATA 2820
 462 R K N R M A L F Q Q L T C V L P I L D N 481

2821 ATCTTTTAAAGGCCAATGTAATTAATAAACAGGAACATGATATTATTAACAAAAAACAC 2880
 482 L L K A N V I N K Q E H D I I K Q K T Q 501

2881 AGATACCTTTACAAGCGAGAGAACTGATTGATACCATTTTGGTTAAAGGAAATGCTGCGG 2940
 502 I P L Q A R E L I D T I L V K G N A A A 521

2941 CCAACATCTTCAAAAAGTGTCTAAAAGAAATTGACTCTACATTGTATAAGAACTTATTG 3000
 522 N I F K N C L K E I D S T L Y K N L F V 541

3001 TGGATAAGAATATGAAGTATATCCCAACAGAAGATGTTTCAGTCTGTCACTGGAAGAAC 3060
 542 D K N M K Y I P T E D V S G L S L E E Q 561

Fig. 3 (cont.)

3061 AATTGAGGAGGTTGCAAGAAGAACGAACTTGTAAGTGTGTATGGACAAAGAAGTTTCTG 3120
562 L R R L Q E E R T C K V C M D K E V S V 581

3121 TTGTATTTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCCTTCTCTAAGAA 3180
582 V F I P C G H L V V C Q E C A P S L R K 601

3181 AATGCCCTATTTGCAGGGGTATAATCAAGGGTACTGTTTCGTACATTTCTCTCTTAAAGAA 3240
602 C P I C R G I I K G T V R T F L S * 618

3241 AAATAGTCTATATTTTAACTGCATAAAAAGGTCTTTAAATATTGTTGAACACTTGAAG 3300
3301 CCATCTAAAGTAAAAAGGGAATTATGAGTTTTTCAATTAGTAACATTCATGTTCTAGTCT 3360
3361 GCTTTGGTACTAATAATCTTGTCTGAAAAGATGGTATCATATATTTAATCTTAATCTG 3420
3421 TTTATTTACAAGGGAAGATTTATGTTTGGTGAACATATATTAGTATGTATGTGTACCTAAG 3480
3481 GGAGTAGTGTCACTGCTTGTATGCATCATTTTCAGGAGTTACTGGATTGTTGTTCTTTC 3540
3541 AGAAAGCTTTGAATACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACCTCTGGAG 3600
3601 TTCATCAGAGTTATGGTGCCGAATTGTCTTGGTGCTTTTCACTTGTGTTTTAAATAAG 3660
3661 GATTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTGCTTTAAAA 3720
3721 AGAAAAAAAAAA 3732

Fig. 3 (cont.)

106007 " 0054650

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SEQ. ID 9-1 ATTTTAAATTGATGCATTAACATTCTAAACATTTCATCTGTTTTTAAATAGTAAAAATT 60
61 GAACTTTGCCCTTGAATATGTAATGATTCATTATAACAATTATGCATAGTCTTTAATAATC 120
121 TGCATATTTTATGCTGCTTTCATGTTTTTCCTAATTAATGACTTCACATGTTTAATATTT 180
181 ATAATTTTCTGTCATAGTTTCCATATTTATATAAAATGAATACTTAAGATCAGTAATTC 240
241 TGCTCTGTTTGTATATACTATTTTCCATCAAAAGACAAAATGGGACTGAGGTTGAGGC 300
301 TCGTTGCTAAAGCACTTTCCTAAAATGCAAAAGGCCCTATGATGGATCCCTAGTACTTAT 360
361 TTAAGTGAGAGAGAAACAGGCTGGGGGTGTAGGTCTGTTAGAGCATGTGTTTGGCATTAT 420
421 GTGAAGCCCAACACTAAAAAAGGAGAACAAACAAAGCGCAGACTTTAAACTCAAGTG 480
481 GTTTGGTAATGTACGACTCTACTGTTTAGAATTAATAATGTGTCTTAGTTATTGTGCCATT 540
541 ATTTTATGTCATCACTGGATAATATATTAGTGCTTAGTATCAGAAATAGTCCTTATGCT 600
601 TTGTGTTTTGAAGTTCCTAATGCAATGTTCTCTTTCTAGAAAAGGTGGACAAGTCCTATT 660
661 TTCCAGAGAAGATGACTTTTAACAGTTTTGAAGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
SEQ. ID 10-1 M T F N S F E G T R T F V L A D T 17
721 CCAATAAGGATGAAGAATTTGTAGAAGAGTTTAATAGATTAAAAACATTTGCTAACTTCC 780
18 N K D E E F V E E F N R L K T F A N F P 37
781 CAAGTAGTAGTCCTGTTTCAGCATCAACATTGGCGCGAGCTGGGTTTCTTTATACCGGTG 840
38 S S S P V S A S T L A R A G F L Y T G E 57
841 AAGGAGACACCGTGCAATGTTTCAGTTGTCATGCGGCAATAGATAGATGGCAGTATGGAG 900
58 G D T V Q C F S C H A A I D R W Q Y G D 77
901 ACTCAGCTGTTGGAAGACACAGGAGAATATCCCCAAATTGCAGATTTATCAATGGTTTTT 960
78 S A V G R H R R I S P N C R F I N G F Y 97
961 ATTTTGAAAATGGTGTGTCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAAAT 1020
98 F E N G A A Q S T N P G I Q N G Q Y K S 117
1021 CTGAAAATGTTGGGAAATAGAAATCCTTTTGGCCCTGACAGGCCACCTGAGACTCATG 1080
118 E N C V G N R N P F A P D R P P E T H A 137
1081 CTGATTATCTCTTGAGAACTGGACAGGTTGTAGATATTTTACAGACACCATATACCCGAGGA 1140
138 D Y L L R T G Q V V D I S D T I Y P R N 157
1141 ACCCTGCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTTTCAAGTGGCCGGACTATG 1200
158 P A M C S E E A R L K S F Q N W P D Y A 177
1201 CTCATTTAACCCCCAGAGAGTTAGCTAGTGCTGGCCTCTACTACACAGGGGCTGATGATC 1260
178 H L T P R E L A S A G L Y Y T G A D D Q 197
1261 AAGTGCAATGCTTTTGTGTGGGGGAAAATGAAAATTTGGGAACCCCTGTGATCGTGCCT 1320
198 V Q C F C C G G K L K N W E P C D R A W 217
1321 GGTGAGAACACAGGAGACACTTCCCAATTGCTTTTTTGTGTTTGGGCCGGAACGTTAATG 1380
218 S E H R R H F P N C F F V L G R N V N V 237
1381 TTCGAAGTGAATCTGGTGTGAGTTCTGATAGGAATTTCCCAAATTCACAACTCTCCAA 1440
238 R S E S G V S S D R N F P N S T N S P R 257
1441 GAAATCCAGCCATGGCAGAATATGAAGCACGGATCGTTACTTTTGAACATGGACATCCT 1500
258 N P A M A E Y E A R I V T F G T W T S S 277

Fig. 4

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1501 CAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCGATAAAG 1560
 278 V N K E Q L A R A G F Y A L G E G D K V 297

1561 TGAAGTGCTTCCACTGTGGAGGAGGGCTCACGGATTGGAAGCCAAGTGAAGACCCCTGGG 1620
 298 K C F H C G G G L T D W K P S E D P W D 317

1621 ACCAGCATGCTAAGTGCTACCCAGGGTGCAAATACCTATTGGATGAGAAGGGGCAAGAAT 1680
 318 Q H A K C Y P G C K Y L L D E K G Q E Y 337

1681 ATATAAATAATATTCATTTAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAA 1740
 338 I N N I H L T H P L E E S L G R T A E K 357

1741 AAACACCACCGCTAACTAAAAAATCGATGATACCATCTTCCAGAATCCTATGGTGCAAG 1800
 358 T P P L T K K I D D T I F Q N P M V Q E 377

1801 AAGCTATACGAATGGGATTTAGCTTCAAGGACCTTAAGAAAACAATGGGAAGAAAAAATCC 1860
 378 A I R M G F S F K D L K K T M E E K I Q 397

1861 AAACATCCGGGAGCAGCTATCTATCACTTGAGGTCCTGATTGCAGATCTTGTGAGTGCTC 1920
 398 T S G S S Y L S L E V L I A D L V S A Q 417

1921 AGAAAGATAATACGGAGGATGAGTCAAGTCAAACCTTATTGCAGAAAGACATTAGTACTG 1980
 418 K D N T E D E S S Q T S L Q K D I S T E 437

1981 AAGAGCAGCTAAGGCGCCTACAAGAGGAGAAGCTTTCCAAAATCTGTATGGATAGAAATA 2040
 438 E Q L R R L Q E E K L S K I C M D R N I 457

2041 TTGCTATCGTTTTTTTTTCTTGTGGACATCTGGCCACTTGTAACAGTGTGCAGAAGCAG 2100
 458 A I V F F P C G H L A T C K Q C A E A V 477

2101 TTGACAAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAAAATTTTATGTCTT 2160
 478 D K C P M C Y T V I T F N Q K I F M S * 496

2161 AGTGGGGCACCACATGTTATGTTCTTCTTGCTCTAATTGAATGTGTAATGGGAGCGAACT 2220
 2221 TTAAGTAATCCTGCATTTGCATTCCATTAGCATCCTGCTGTTTCCAAATGGAGACCAATG 2280
 2281 CTAACAGCACTGTTTCCGTCTAAACATTCAATTTCTGGATCTTTTCGAGTTATCAGCTGTA 2340
 2341 TCATTTAGCCAGTGTCTTACTCGATTGAAACCTTAGACAGAGAAGCATTATAGCTTTT 2400
 2401 CACATGTATATTGGTAGTACACTGACTTGATTCTATATGTAAGTGAATTCATCACCTGC 2460
 2461 ATGTTTCATGCCTTTTGCATAAGCTTAACAAATGGAGTGTTCTGTATAAGCATGGAGATG 2520
 2521 TGATGGAATCTGCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAAGAACTGCCCA 2580
 2581 CGCTGCTGGGAGGATAAAGATTGTTTTAGATGCTCACTTCTGTGTTTTAGGATTCTGCCC 2640
 2641 ATTTACTTGAATTTATTGGAGTTATAATGTACTTATATGATATTTCCGAA 2691

Fig. 4 (cont.)

Fig. 5

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1261 TGCTCAGAATCAAAGGCCAAGAATTTGTCTAGCCAAGTTCAAGCTGGCTATCCTCATCTAC 1320
 321 L R I K G Q E F V S Q V Q A G Y P H L L 340
 1321 TTGAGCAGCTATTATCTACGTCAGACTCCCCAGAAGATGAGAATGCAGACGCAGCAATCG 1380
 341 E Q L L S T S D S P E D E N A D A A I V 360
 1381 TGCATTTTGGCCCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCACGCCTGTGGTTA 1440
 361 H F G P G E S S E D V V M M S T P V V K 380
 1441 AAGCAGCCTTGGAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTTCAGCGGCAGA 1500
 381 A A L E M G F S R S L V R Q T V Q R Q I 400
 1501 TCCTGGCCACTGGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATG 1560
 401 L A T G E N Y R T V S D L V I G L L D A 420
 1561 CAGAAGACGAGATGAGAGAGGAGCAGATGGAGCAGGCGGCCGAGGAGGAGGAGTCAATG 1620
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 1621 ATCTAGCACTAATCCGGAAGAACAAATGGTGCTTTTCCAACATTTGACGTGTGTGACAC 1680
 441 L A L I R K N K M V L F Q H L T C V T P 460
 1681 CAATGCTGTATTGCCTCCTAAGTGCAAGGGCCATCACTGAACAGGAGTGCAATGCTGTGA 1740
 461 M L Y C L L S A R A I T E Q E C N A V K 480
 1741 AACAGAAACCACACACCTTACAAGCAAGCACACTGATTGATACTGTGTTAGCAAAAGGAA 1800
 481 Q K P H T L Q A S T L I D T V L A K G N 500
 1801 AACTGTCAGCAACCTCATTTCAGAACTCCCTTCGGGAAATTGACCCTGCGTTATACAGAG 1860
 501 T A A T S F R N S L R E I D P A L Y R D 520
 1861 ATATATTTGTGCAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAA 1920
 521 I F V Q Q D I R S L P T D D I A A L P M 540
 1921 TGGAAGAACAGTTGCGGAAACTCCAGGAGGAAAGAATGTGTAAAGTGTGTATGGACCGAG 1980
 541 E E Q L R K L Q E E R M C K V C M D R E 560
 1981 AGGTATCCATCGTGTTCATTCCCTGTGGCCATCTGGTCTGTGTGCAAAGACTGCGCTCCCT 2040
 561 V S I V F I P C G H L V V C K D C A P S 580
 2041 CTCTGAGGAAGTGTCCCATCTGTAGAGGGACCATCAAGGGCACAGTGCGCACATTTCTCT 2100
 581 L R K C P I C R G T I K G T V R T F L S 600
 2101 CCTGAACAAGACTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACTGTCACT 2160
 *
 2161 CCCAGCTCCATTCGGAACCTTGAGGCCAGCCTGGATAGCACGAGACACCGCCAAACACACA 2220
 2221 AATATAACATGAAAACTTTTGTCTGAAGTCAAGAATGAATGAATTACTTATATAATAA 2280
 2281 TTTTAATTGGTTTCTTAAAGTGCTATTGTTCCTCAACTCAGAAAATTGTTTTCTGTAA 2340
 2341 ACATATTTACATACTACCTGCATCTAAAGTATTCATATATTCATATATTCAGATGTCATG 2400
 2401 AGAGAGGGTTTTGTCTTGTTCCTGAAAAGCAGGGATTGCCTGCACTCCTGAAATTCTCA 2460
 2461 GAAAGATTTACAATGTTGGCATTATGGTTTCAGAACTAGAATCTTCTCCGTTGCTTTA 2520
 2521 AGAACCGGGAGCACAGATGTCCATGTGTTTTATGTATAGAAATTCCTGTTATTTATTGGA 2580
 2581 TGACATTTTAGGGATATGAAATTTTTATAAAGAATTTGTGAGAAAAAGTTAATAAAGCAA 2640
 2641 CATAATTACCTCTTTTTTTTTTAAAGAAAAA 2676

Fig. 5 (cont.)

Fig. 6

1561 ACACTCTGCTCGATTGAGGACATTTCTGTACTGGCCACCTAGTGTTCTGTTCAGCCCCGA 1620
 262 H S A R L R T F L Y W P P S V P V Q P E 281
 1621 GCAGCTTGCAAGTGCTGGATTCTATTACGTGGATCGCAATGATGATGTCAAGTGCTTTTG 1680
 282 Q L A S A G F Y Y V D R N D D V K C F C 301
 1681 TTGTGATGGTGGCTTGAGATGTTGGGAACCTGGAGATGACCCCTGGATAGAACACGCCAA 1740
 302 C D G G L R C W E P G D D P W I E H A K 321
 1741 ATGGTTTCCAAGTGTGAGTTCTTGATACGGATGAAGGGTCAGGAGTTTGTGATGAGAT 1800
 322 W F P R C E F L I R M K G Q E F V D E I 341
 1801 TCAAGCTAGATATCCTCATCTTCTTGAGCAGCTGTTGTCCACTTCAGACACCCCAGGAGA 1860
 342 Q A R Y P H L L E Q L L S T S D T P G E 361
 1861 AGAAAATGCTGACCCTACAGAGACAGTGGTGCATTTTGGCCCTGGAGAAAGTTGAAAGA 1920
 362 E N A D P T E T V V H F G P G E S S K D 381
 1921 TGTCGTCATGATGAGCACGCCTGTGGTTAAAGCAGCCTTGGAATGGGCTTCAGTAGGAG 1980
 382 V V M M S T P V V K A A L E M G F S R S 401
 1981 CCTGGTGAGACAGACGGTTCAGCGGCAGATCCTGGCCACTGGTGAGAACTACAGGACCGT 2040
 402 L V R Q T V Q R Q I L A T G E N Y R T V 421
 2041 CAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGAGAGAAGAGAAGAGGAGAAGGA 2100
 422 N D I V S V L L N A E D E R R E E E K E 441
 2101 AAGACAGACTGAAGAGATGGCATCAGTGAAGTATCACTGATTGCGAAGAATAGAATGGC 2160
 442 R Q T E E M A S G D L S L I R K N R M A 461
 2161 CCTCTTTCAACAGTTGACACATGTCCTTCCTATCCTGGATAATCTTCTTGAGGCCAGTGT 2220
 462 L F Q Q L T H V L P I L D N L L E A S V 481
 2221 AATTACAAAACAGGAACATGATATTATTAGACAGAAAACACAGATACCCTTACAAGCAAG 2280
 482 I T K Q E H D I I R Q K T Q I P L Q A R 501
 2281 AGAGCTTATTGACACCGTTTTAGTCAAGGGAAATGCTGCAGCCAACATCTTCAAAAACCTC 2340
 502 E L I D T V L V K G N A A A N I F K N S 521
 2341 TCTGAAGGAAATTGACTCCACGTTATATGAAAACCTATTTGTGGAAAAGAATATGAAGTA 2400
 522 L K E I D S T L Y E N L F V E K N M K Y 541
 2401 TATTCCAACAGAAGACGTTTCAGGCTTGTGATTGGAAGAGCAGTTGCGGAGATTACAAGA 2460
 542 I P T E D V S G L S L E E Q L R R L Q E 561
 2461 AGAACGAACTTGCAAAGTGTGTATGGACAGAGAGGTTTCTATTGTGTTTATTCCGTGTGG 2520
 562 E R T C K V C M D R E V S I V F I P C G 581
 2521 TCATCTAGTAGTCTGCCAGGAATGTGCCCTTCTCTAAGGAAGTGCCCATCTGCAGGGG 2580
 582 H L V V C Q E C A P S L R K C P I C R G 601
 2581 GACAATCAAGGGGACTGTGCGCACATTTCTCTCATGAGTGAAGAATGGTCTGAAAGTATT 2640
 602 T I K G T V R T F L S * 612

Fig. 6 (cont.)

2641 GTTGGACATCAGAAGCTGTCAGAACAAAGAATGAACTACTGATTTTCAGCTCTTCAGCAGG 2700
2701 ACATTCTACTCTCTTTCAAGATTAGTAATCTTGCTTTATGAAGGGTAGCATTGTATATTT 2760
2761 AAGCTTAGTCTGTTGCAAGGGAAGGTCTATGCTGTTGAGCTACAGGACTGTGTCTGTTCC 2820
2821 AGAGCAGGAGTTGGGATGCTTGCTGTATGTCCTTCAGGACTTCTTGGATTGGAATTTGT 2880
2881 GAAAGCTTTGGATTAGGTGATGTGGAGCTCAGAAATCCTGAAACCAGTGGCTCTGGTAC 2940
2941 TCAGTAGTTAGGGTACCCTGTGCTTCTTGGTGCTTTTCCTTTCTGGAAAATAAGGATTTT 3000
3001 TCTGCTACTGGTAAATATTTTCTGTTTGTGAGAAATATATTAAAGTGTTCCTTTAAAGG 3060
3061 CGTGCAATCATTGTAGTGTGTGCAGGGATGTATGCAGGCAAAACACTGTGTATATAATAAA 3120
3121 TAAATCTTTTAAAAAGTGTAACAAAAA 3151

Fig. 6 (cont.)

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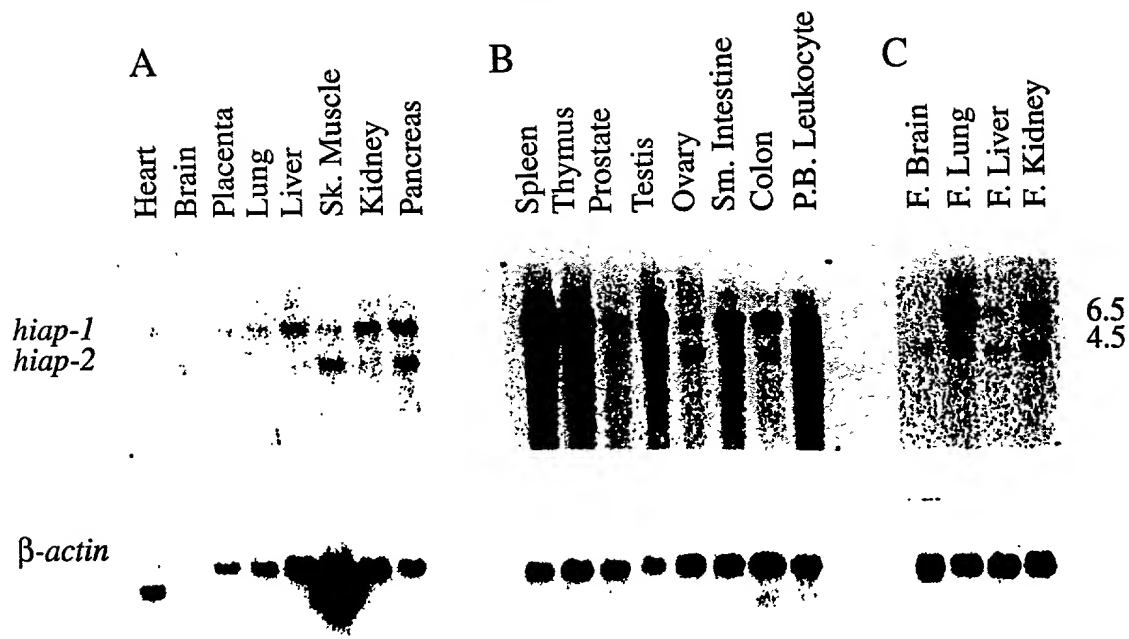


Fig. 7

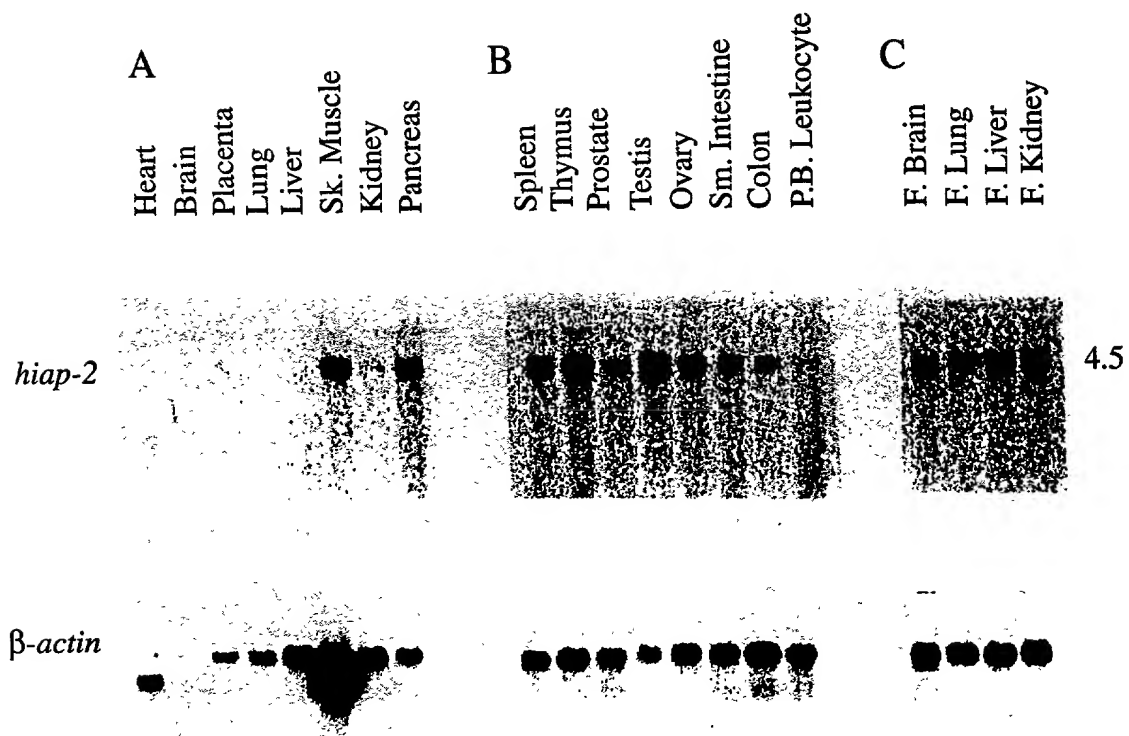


Fig. 8

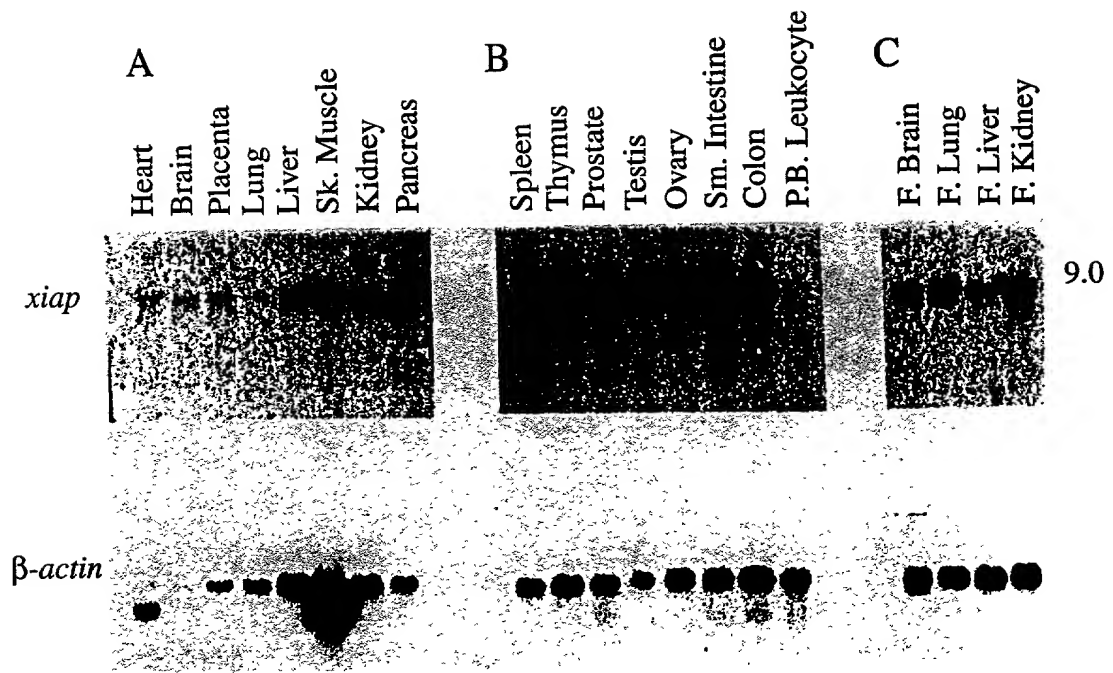


Fig. 9

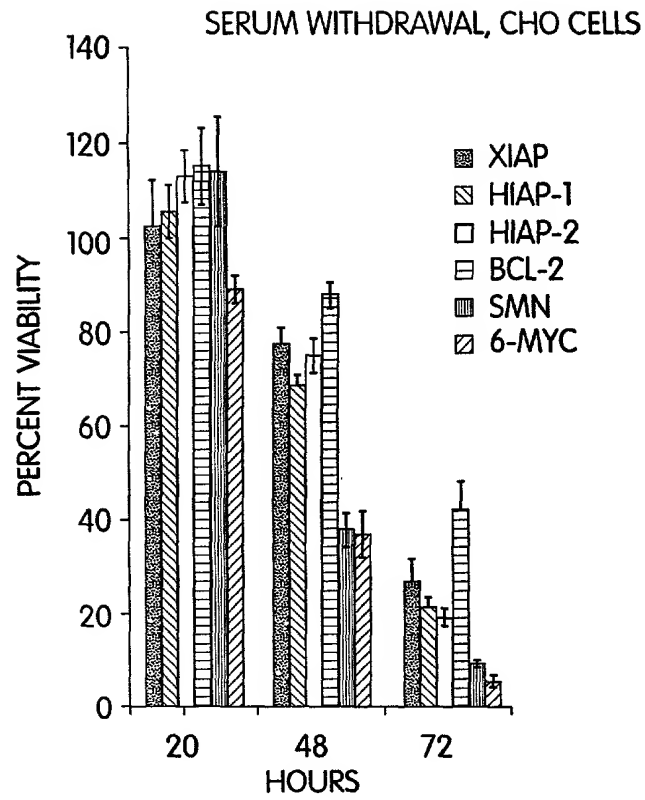


Fig. 10A

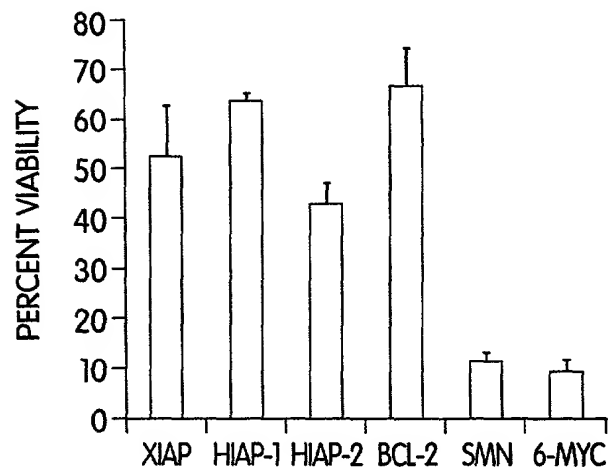
MENADIONE (20 μ M), CHO CELLS. 24hr SURVIVAL

Fig. 10B

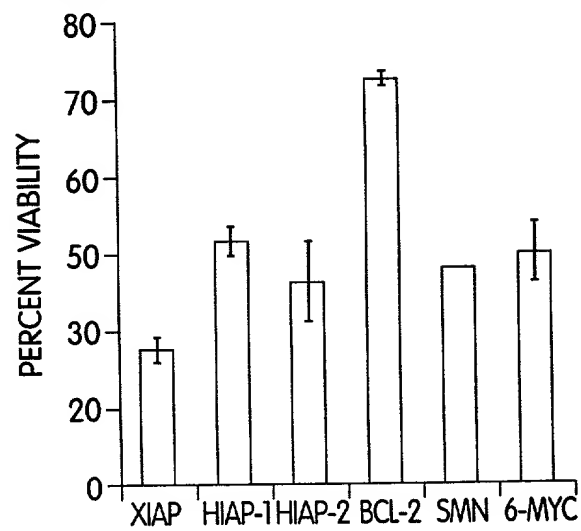
STAUROSPORINE (1 μ M), RAT-1 CELLS, 24 HOUR SURVIVAL

Fig. 10C

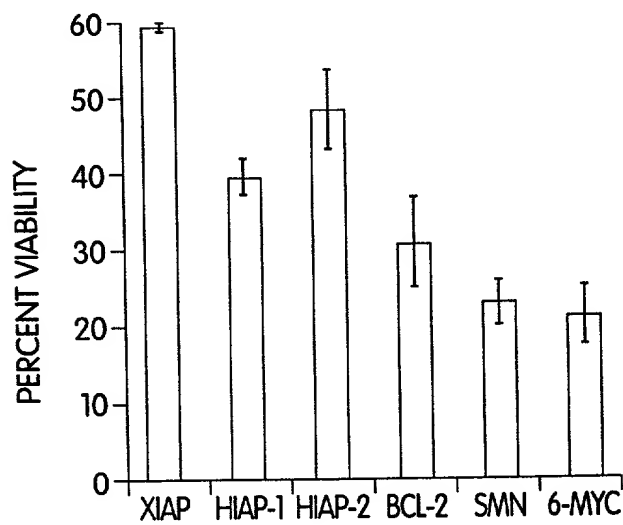
MENADIONE (10 μ M), RAT-1 CELLS, 18 HOUR SURVIVAL

Fig. 10D

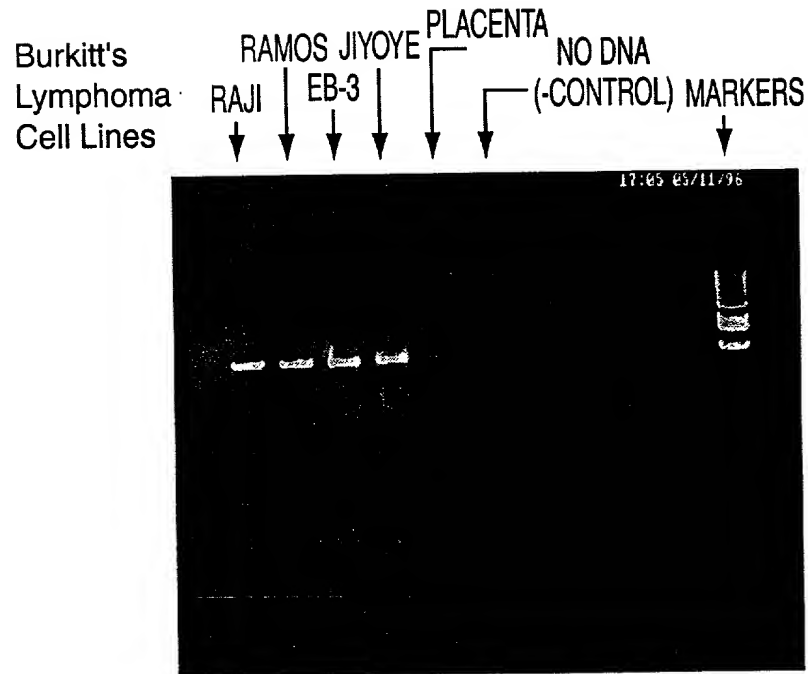


Fig. 11

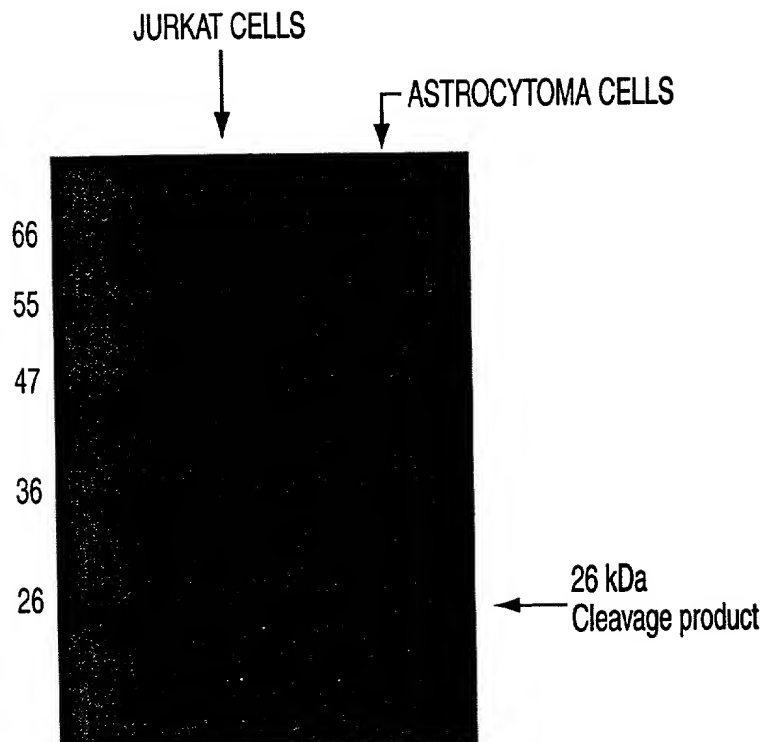


Fig. 12

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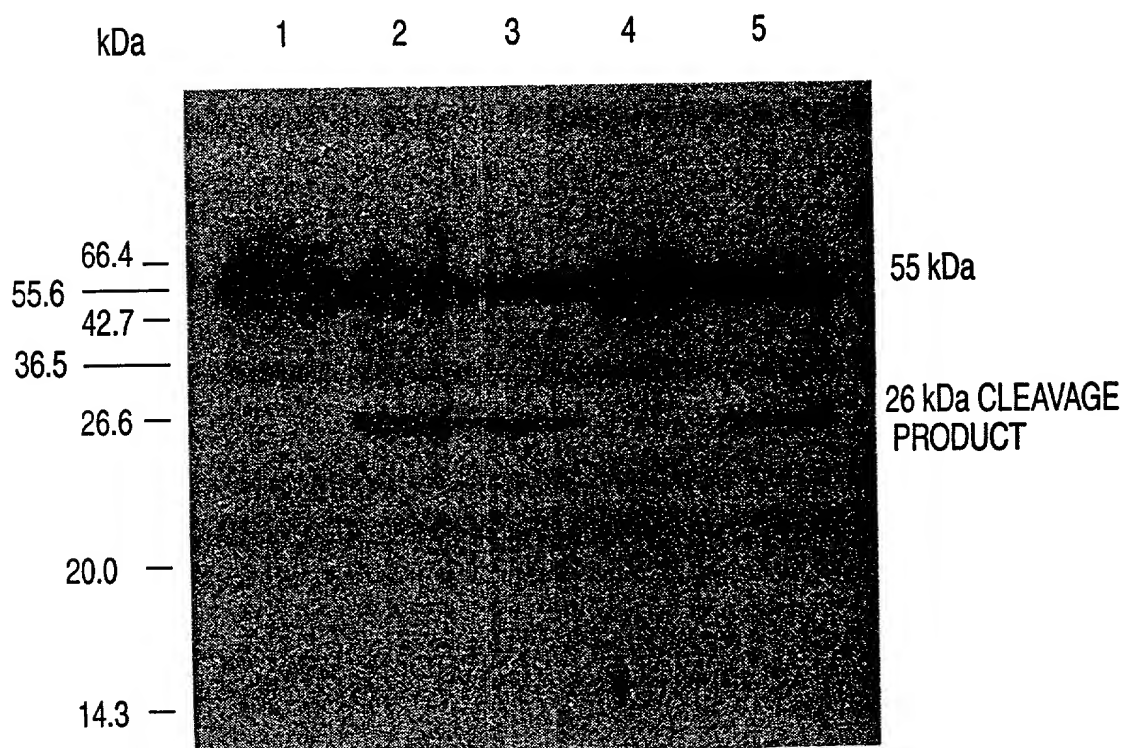


Fig. 13

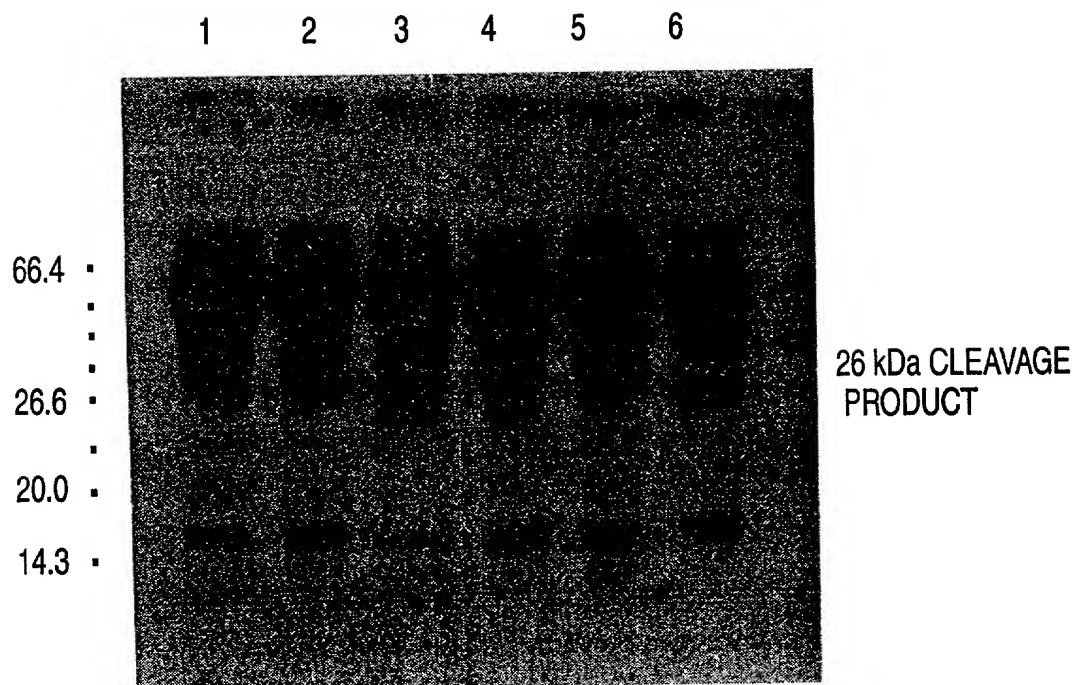


Fig. 14

TOPDOT " 26572650

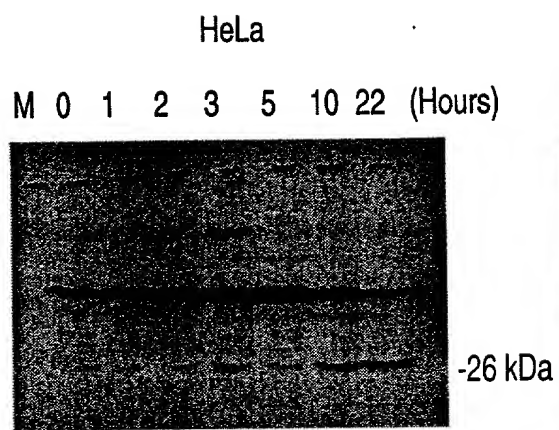


Fig. 15A

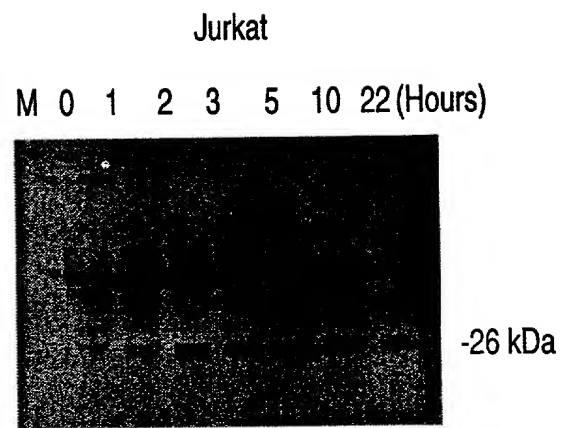


Fig. 15B

3 HOURS
HOURS 0 3 7 Cyto. Nucl.

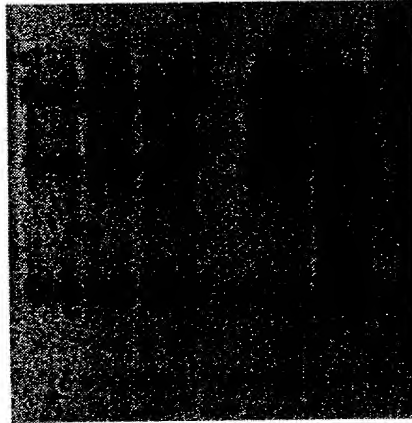
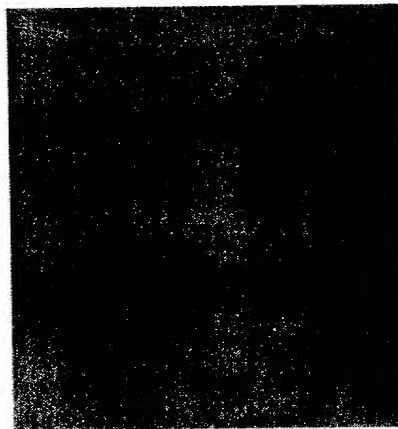


Fig. 16A

3 HOURS
MARKERS 0 3 7 Cyto. Nucl.

97.2 —
55.6 — 66.4 —
36.5 — 42.7 —
26.6 —



← 55 kDa

← 25 kDa

Fig. 16B

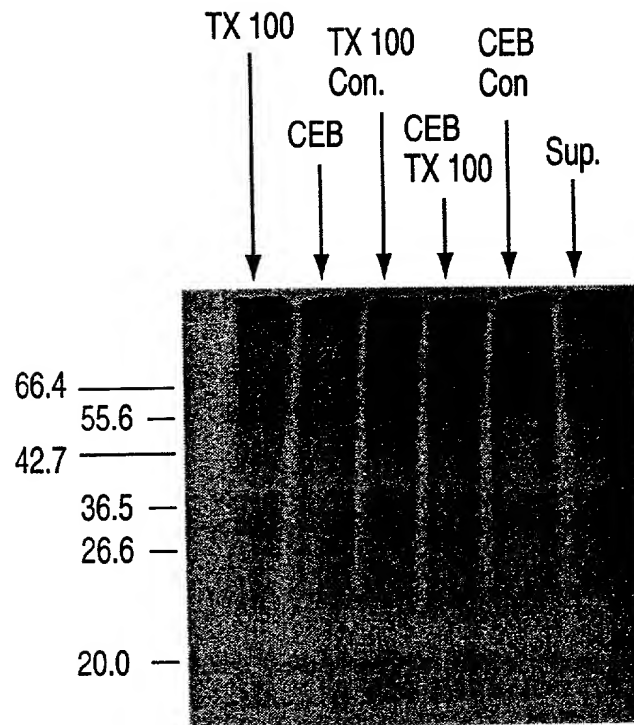


Fig. 17

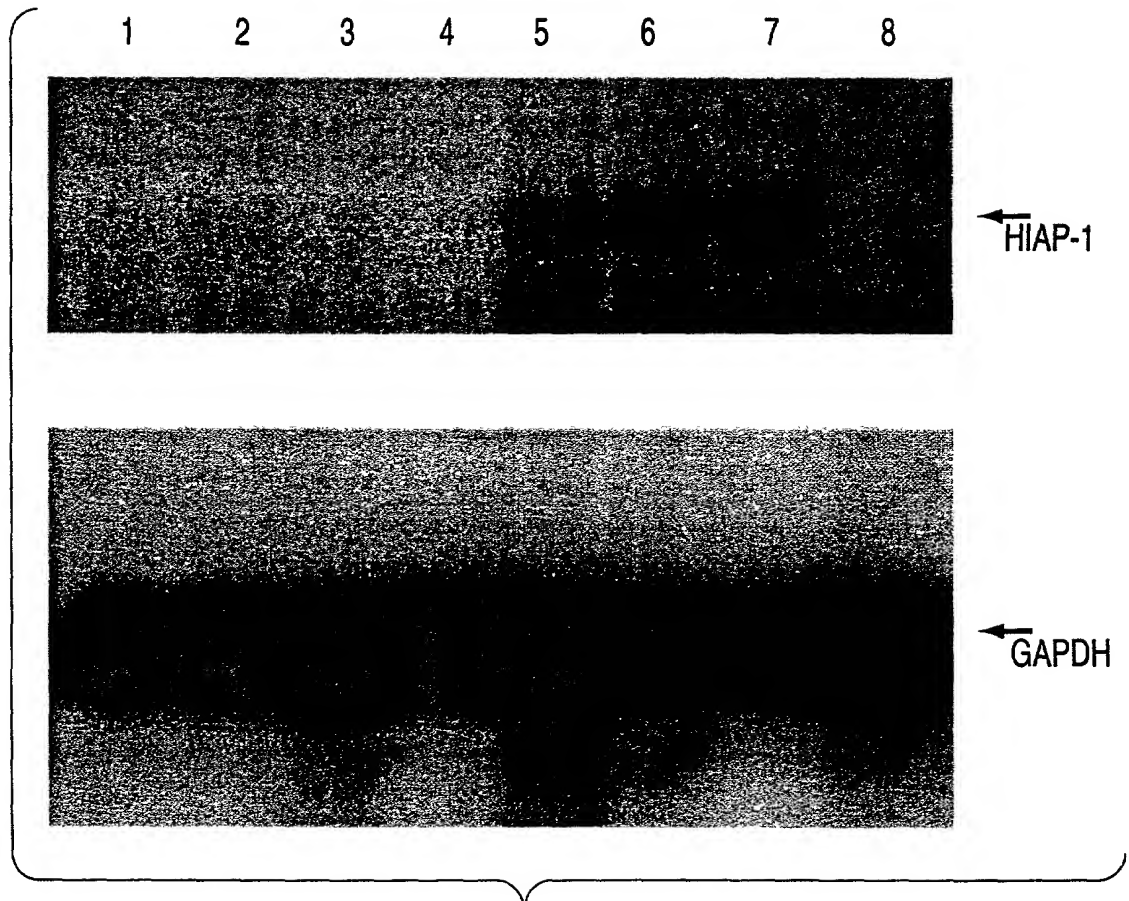


Fig. 18

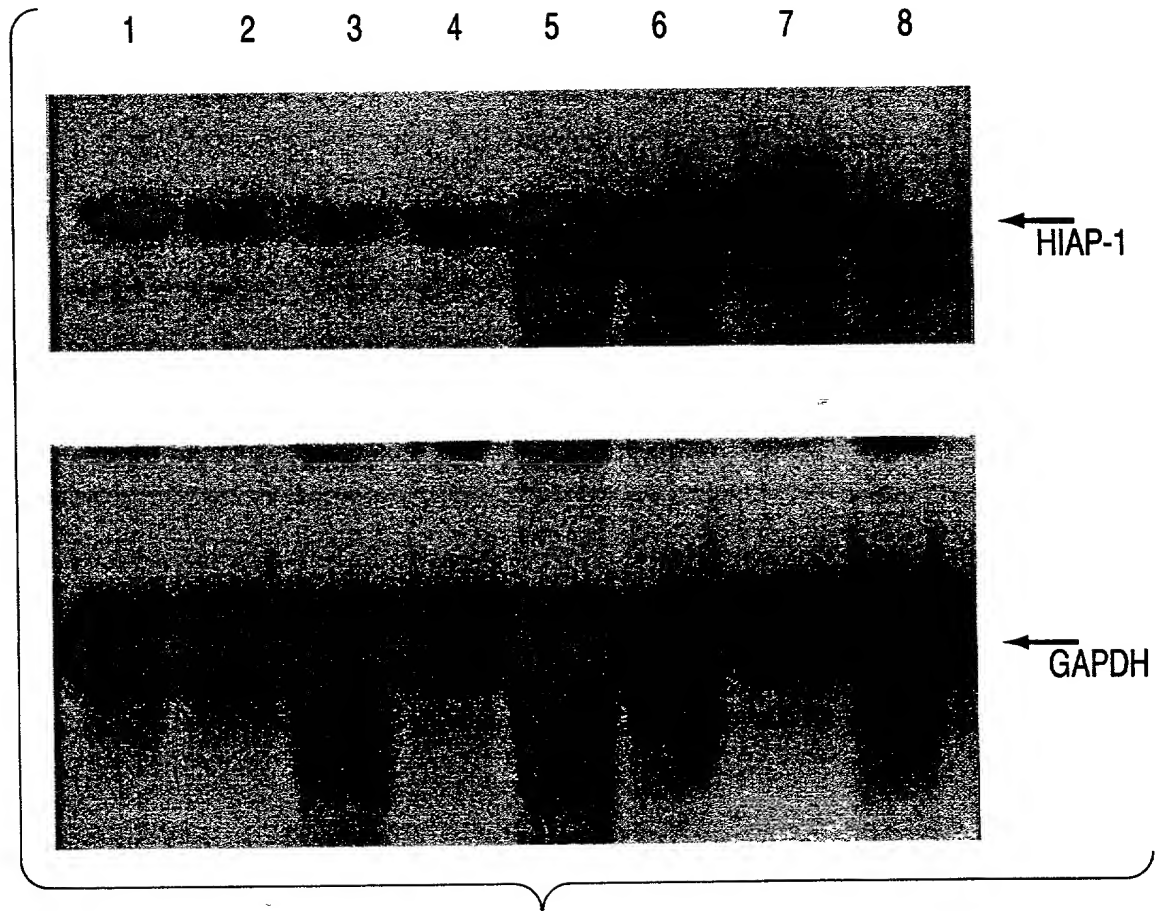


Fig. 19

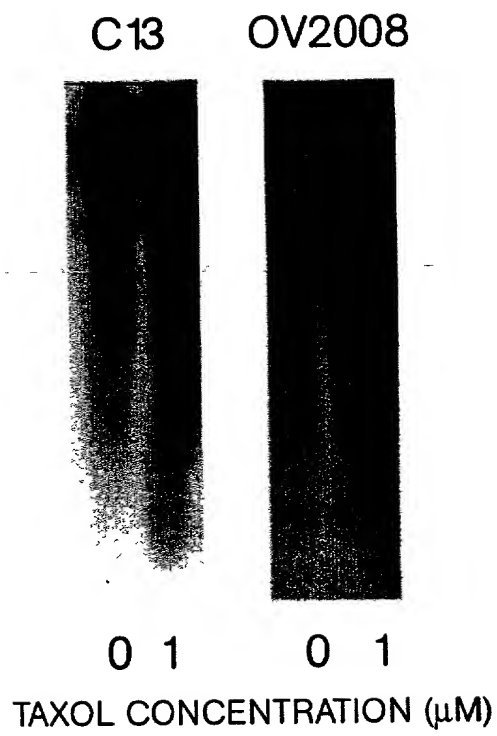


Fig. 20

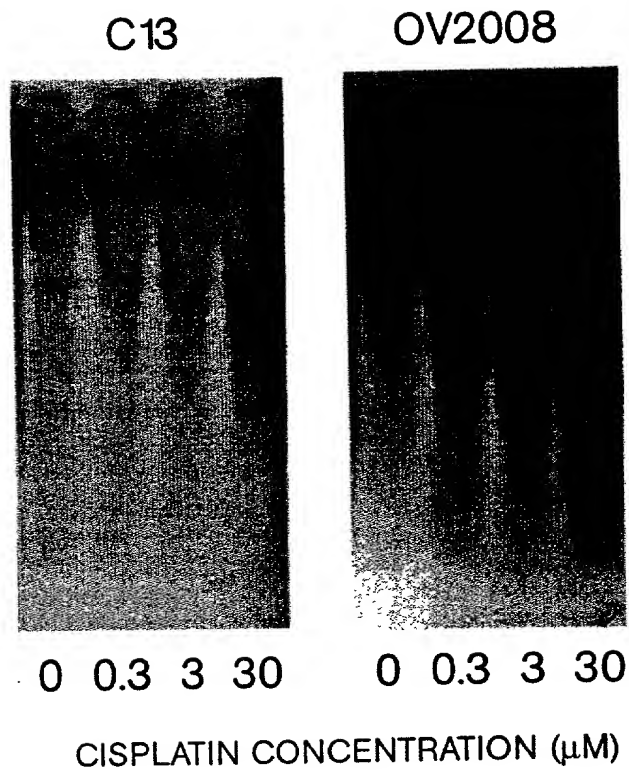


Fig. 21

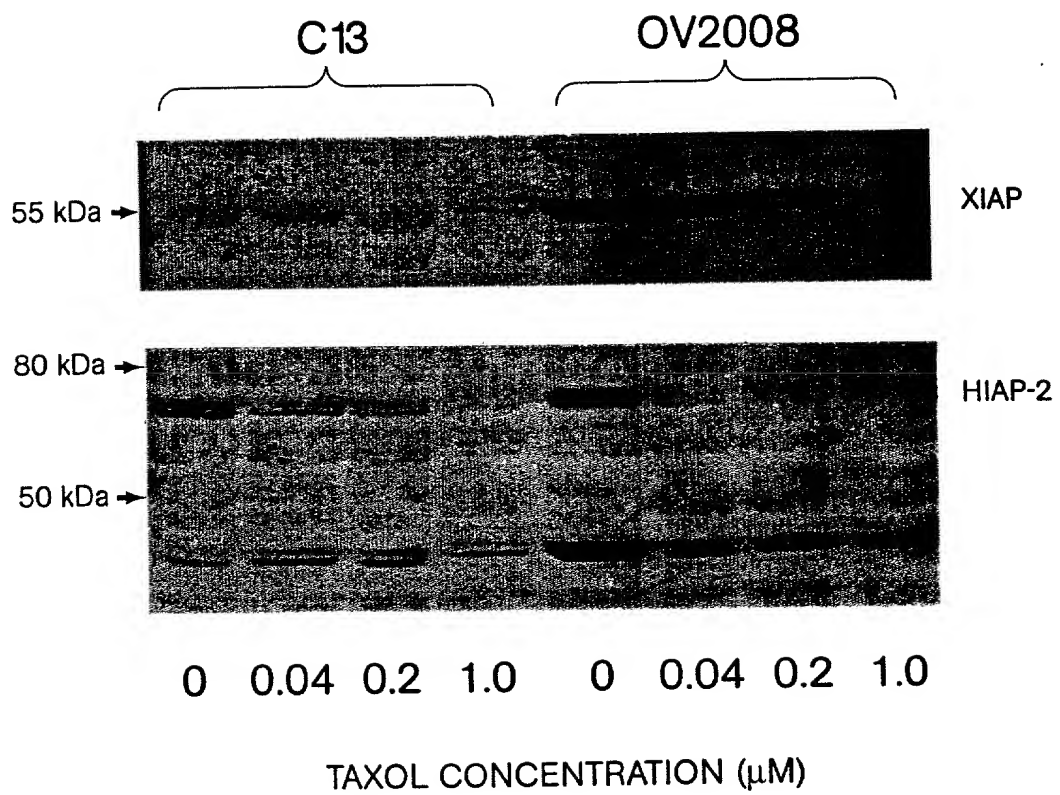


Fig. 22

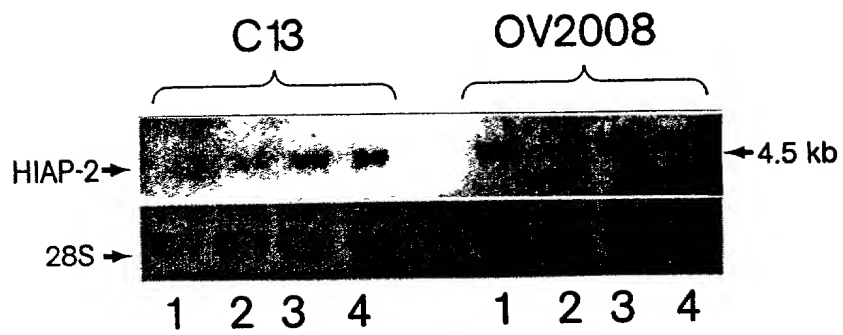


Fig. 23A

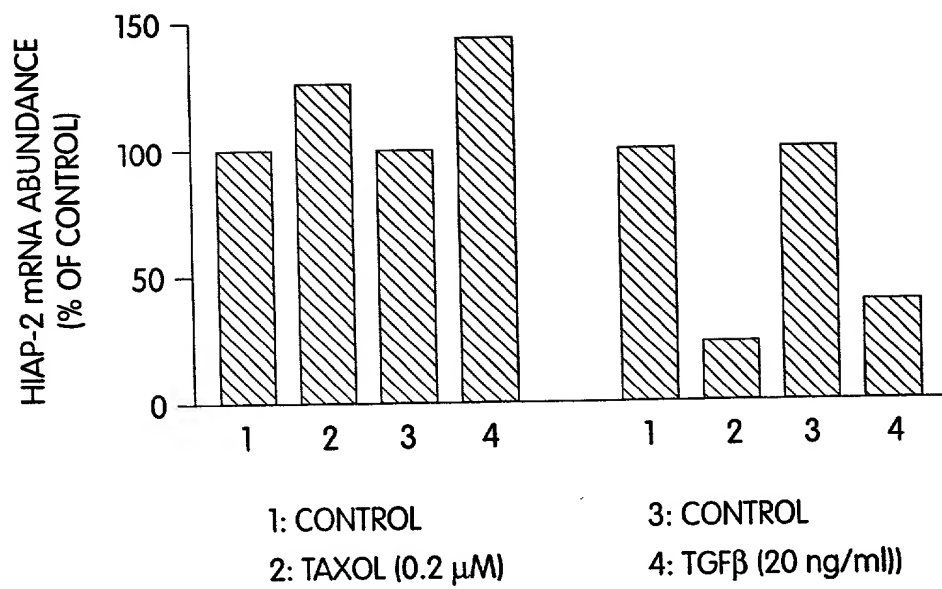


Fig. 23B

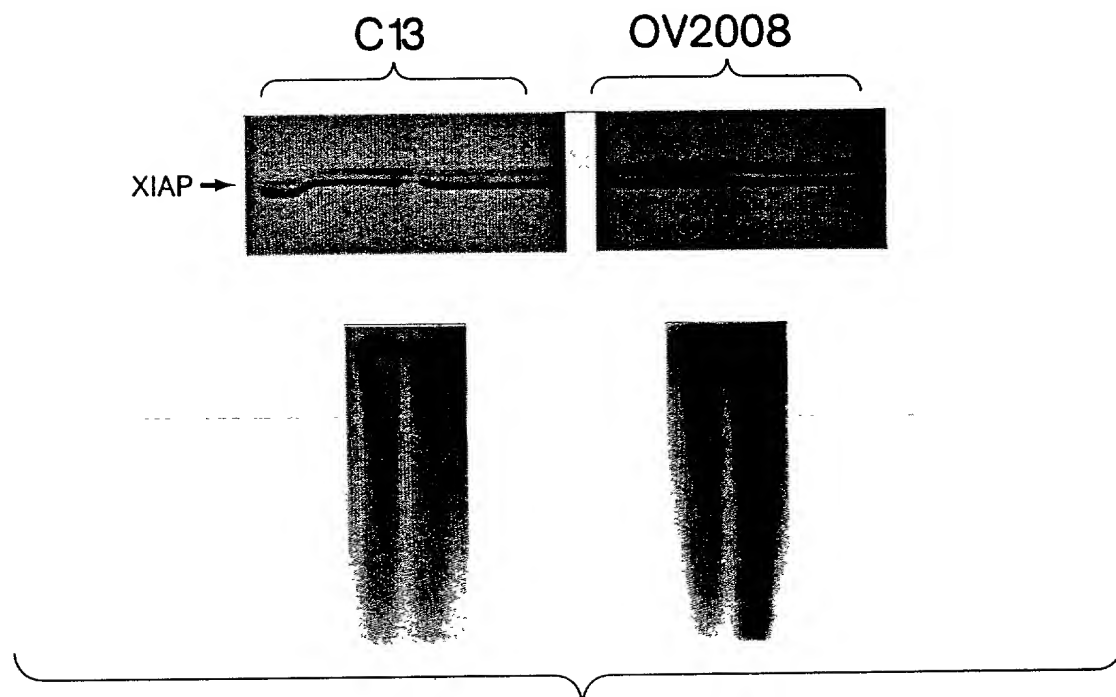


Fig. 24A

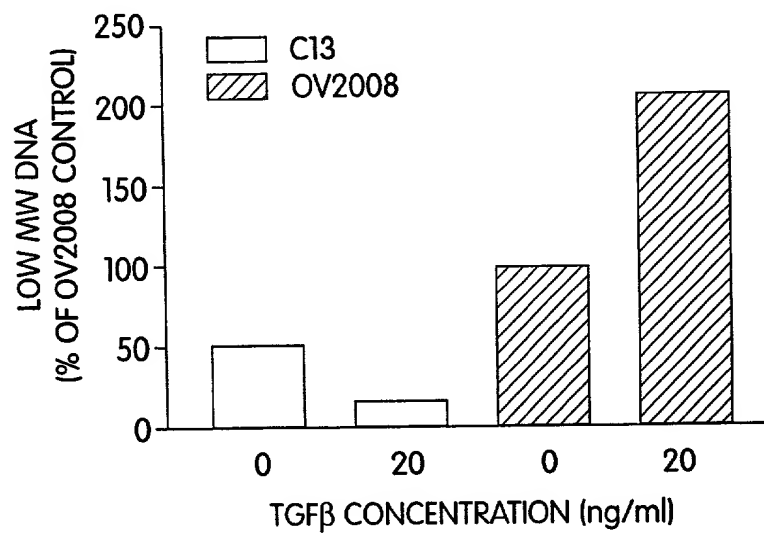


Fig. 24B